

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/806,194

DATE: 04/04/2001

TIME: 11:19:20

Input Set : A:\6177.txt

Output Set: N:\CRF3\04042001\I806194.raw

```

59 gctcccagat gccttctaga ttactgtct ttgattctt gattttcaag ctttcaaattc 1740
60 ctccctactt ccaagaaaaa taattaaaaa aaaaacttca ttctaaacca aaaaaaaaaa 1800
61 aaaa 1804
64 <210> SEQ ID NO: 2
65 <211> LENGTH: 518
66 <212> TYPE: PRT
67 <213> ORGANISM: Homo sapiens
69 <400> SEQUENCE: 2
70 Met Gly Ala Leu Ala Arg Ala Leu Leu Pro Leu Leu Ala Gln Trp
71 1 5 10 15
73 Leu Leu Arg Ala Ala Pro Glu Leu Ala Pro Ala Pro Phe Thr Leu Pro
74 20 25 30
76 Leu Arg Val Ala Ala Ala Thr Asn Arg Val Val Ala Pro Thr Pro Gly
77 35 40 45
79 Pro Gly Thr Pro Ala Glu Arg His Ala Asp Gly Leu Ala Leu Ala Leu
80 50 55 60
82 Glu Pro Ala Leu Ala Ser Pro Ala Gly Ala Ala Asn Phe Leu Ala Met
83 65 70 75 80
85 Val Asp Asn Leu Gln Gly Asp Ser Gly Arg Gly Tyr Tyr Leu Glu Met
86 85 90 95
88 Leu Ile Gly Thr Pro Pro Gln Lys Leu Gln Ile Leu Val Asp Thr Gly
89 100 105 110
91 Ser Ser Asn Phe Ala Val Ala Gly Thr Pro His Ser Tyr Ile Asp Thr
92 115 120 125
94 Tyr Phe Asp Thr Glu Arg Ser Ser Thr Tyr Arg Ser Lys Gly Phe Asp
95 130 135 140
97 Val Thr Val Lys Tyr Thr Gln Gly Ser Trp Thr Gly Phe Val Gly Glu
98 145 150 155 160
100 Asp Leu Val Thr Ile Pro Lys Gly Phe Asn Thr Ser Phe Leu Val Asn
101 165 170 175
103 Ile Ala Thr Ile Phe Glu Ser Glu Asn Phe Phe Leu Pro Gly Ile Lys
104 180 185 190
106 Trp Asn Gly Ile Leu Gly Leu Ala Tyr Ala Thr Leu Ala Lys Pro Ser
107 195 200 205
109 Ser Ser Leu Glu Thr Phe Phe Asp Ser Leu Val Thr Gln Ala Asn Ile
110 210 215 220
112 Pro Asn Val Phe Ser Met Gln Met Cys Gly Ala Gly Leu Pro Val Ala
113 225 230 235 240
115 Gly Ser Gly Thr Asn Gly Gly Ser Leu Val Leu Gly Gly Ile Glu Pro
116 245 250 255
118 Ser Leu Tyr Lys Gly Asp Ile Trp Tyr Thr Pro Ile Lys Glu Glu Trp
119 260 265 270
121 Tyr Tyr Gln Ile Glu Ile Leu Lys Leu Glu Ile Gly Gly Gln Ser Leu
122 275 280 285
124 Asn Leu Asp Cys Arg Glu Tyr Asn Ala Asp Lys Ala Ile Val Asp Ser
125 290 295 300
127 Gly Thr Thr Leu Leu Arg Leu Pro Gln Lys Val Phe Asp Ala Val Val
128 305 310 315 320
130 Glu Ala Val Ala Arg Ala Ser Leu Ile Pro Glu Phe Ser Asp Gly Phe

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131          325          330          335
133 Trp Thr Gly Ser Gln Leu Ala Cys Trp Thr Asn Ser Glu Thr Pro Trp
134          340          345          350
136 Ser Tyr Phe Pro Lys Ile Ser Ile Tyr Leu Arg Asp Glu Asn Ser Ser
137          355          360          365
139 Arg Ser Phe Arg Ile Thr Ile Leu Pro Gln Leu Tyr Ile Gln Pro Met
140          370          375          380
142 Met Gly Ala Gly Leu Asn Tyr Glu Cys Tyr Arg Phe Gly Ile Ser Pro
143 385          390          395          400
145 Ser Thr Asn Ala Leu Val Ile Gly Ala Thr Val Met Glu Gly Phe Tyr
146          405          410          415
148 Val Ile Phe Asp Arg Ala Gln Lys Arg Val Gly Phe Ala Ala Ser Pro
149          420          425          430
151 Cys Ala Glu Ile Ala Gly Ala Ala Val Ser Glu Ile Ser Gly Pro Phe
152          435          440          445
154 Ser Thr Glu Asp Val Ala Ser Asn Cys Val Pro Ala Gln Ser Leu Ser
155          450          455          460
157 Glu Pro Ile Leu Trp Ile Val Ser Tyr Ala Leu Met Ser Val Cys Gly
158 465          470          475          480
160 Ala Ile Leu Leu Val Leu Ile Val Leu Leu Leu Pro Phe Arg Cys
161          485          490          495
163 Gln Arg Arg Pro Arg Asp Pro Glu Val Val Asn Asp Glu Ser Ser Leu
164          500          505          510
166 Val Arg His Arg Trp Lys
167          515
170 <210> SEQ ID NO: 3
171 <211> LENGTH: 2070
172 <212> TYPE: DNA
173 <213> ORGANISM: Homo sapiens
175 <400> SEQUENCE: 3
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177 ggcacccagc acggcatccg gctgcccctg cgcagcggcc tggggggcgc cccctgggg 120
178 ctgcggtgct cccgggagac cgacgaagag cccgaggagc ccggccggag gggcagcttt 180
179 gtggagatgg tggacaacct gaggggcaag tgggggcagg gctactacgt ggagatgacc 240
180 gtgggcagcc ccccgccagc gctcaacatc ctggtggata caggcagcag taactttgca 300
181 gtgggtgctg ccccccaccc ctctctgcat cgctactacc agaggcagct gtccagcaca 360
182 taccgggacc tccggaaggg tgtgtatgtg ccctacaccc agggcaagtg ggaaggggag 420
183 ctgggcaccg acctggtaag catcccccat ggcccacag tcaactgtgc tgccaacatt 480
184 gctgccatca ctgaatcaga caagttcttc atcaacggct ccaactggga aggcattcctg 540
185 gggctggcct atgctgagat tgccaggcct gacgactccc tggagccttt ctttgactct 600
186 ctggtaaagc agaccacagt tcccaacctc ttctccctgc acctttgtgg tgctggcttc 660
187 cccctcaacc agtctgaagt gctggcctct gtcggaggga gcatgatcat tggaggatat 720
188 gaccactcgc tgtacacagg cagtctctgg tatacaccca tccggcggga gtggtattat 780
189 gaggtcatca ttgtgcgggg ggagatcaat ggacaggatc tgaaaatgga ctgcaaggag 840
190 tacaactatg acaagagcat tgtggacagt ggcaccacca accttcgttt gcccaagaaa 900
191 gtgtttgaag ctgcagtc aa atccatcaag gcagcctcct ccacggagaa gttccctgat 960
192 ggtttctggc taggagagca gctgggtgtgc tggcaagcag gcaccacccc ttggaacatt 1020
193 ttcccagtc tctcaactct cctaattgggt gaggttacca accagtcctt ccgcatcacc 1080
194 atccttccgc agcaatacct gcggccagtg gaagatgtgg ccacgtccca agacgactgt 1140

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195 tacaagtttg ccatctcaca gtcattccacg ggcactgtta tgggagctgt tatcatggag 1200
196 ggcttctacg ttgtctttga tcggggccga aaacgaattg gctttgctgt cagcgcttg 1260
197 catgtgcacg atgagttcag gacggcagcg gtggaaggcc cttttgtcac cttggacatg 1320
198 gaagactgtg gctacaacat tccacagaca gatgagtcaa ccctcatgac catagcctat 1380
199 gtcattggctg ccatctgcgc cctcttcatg ctgccactct gcctcatggg gtgtcagtgg 1440
200 cgctgcctcc gctgcctgcg ccagcagcat gatgactttg ctgatgacat ctccctgctg 1500
201 aagtgaggag gcccatgggc agaagataga gattcccctg gaccacacct ccgtgggttca 1560
202 ctttggtcac aagtaggaga cacagatggc acctgtggcc agagcacctc aggaccctcc 1620
203 ccacccacca aatgcctctg ccttgatgga gaaggaaaag gctggcaagg tgggttccag 1680
204 ggactgtacc tgtaggaaac agaaaagaga agaaaagaag actctgctgg cggaataact 1740
205 cttggtcacc tcaaatttaa gtggggaat tctgtgctt gaaacttcag ccctgaacct 1800
206 ttgtccacca ttcttttaaa ttctccaacc caaagtattc ttcttttctt agtttcagaa 1860
207 gtactggcat cacacgcagg ttaccttggc gtgtgtccct gtggtaccct ggcagagaag 1920
208 agaccaagct tgtttccctg ctggccaaag tcagtaggag aggatgcaca gtttgctatt 1980
209 tgcttttagag acagggactg tataaacaag cctaacattg gtgcaaagat tgcctcttga 2040
210 attaaaaaaaa aaaaaaaaaa aaaaaaaaaa 2070
212 <210> SEQ ID NO: 4
213 <211> LENGTH: 501
214 <212> TYPE: PRT
215 <213> ORGANISM: Homo sapiens
217 <400> SEQUENCE: 4
218 Met Ala Gln Ala Leu Pro Trp Leu Leu Leu Trp Met Gly Ala Gly Val
219 1 5 10 15
221 Leu Pro Ala His Gly Thr Gln His Gly Ile Arg Leu Pro Leu Arg Ser
222 20 25 30
224 Gly Leu Gly Gly Ala Pro Leu Gly Leu Arg Leu Pro Arg Glu Thr Asp
225 35 40 45
227 Glu Glu Pro Glu Glu Pro Gly Arg Arg Gly Ser Phe Val Glu Met Val
228 50 55 60
230 Asp Asn Leu Arg Gly Lys Ser Gly Gln Gly Tyr Tyr Val Glu Met Thr
231 65 70 75 80
233 Val Gly Ser Pro Pro Gln Thr Leu Asn Ile Leu Val Asp Thr Gly Ser
234 85 90 95
236 Ser Asn Phe Ala Val Gly Ala Ala Pro His Pro Phe Leu His Arg Tyr
237 100 105 110
239 Tyr Gln Arg Gln Leu Ser Ser Thr Tyr Arg Asp Leu Arg Lys Gly Val
240 115 120 125
242 Tyr Val Pro Tyr Thr Gln Gly Lys Trp Glu Gly Glu Leu Gly Thr Asp
243 130 135 140
245 Leu Val Ser Ile Pro His Gly Pro Asn Val Thr Val Arg Ala Asn Ile
246 145 150 155 160
248 Ala Ala Ile Thr Glu Ser Asp Lys Phe Phe Ile Asn Gly Ser Asn Trp
249 165 170 175
251 Glu Gly Ile Leu Gly Leu Ala Tyr Ala Glu Ile Ala Arg Pro Asp Asp
252 180 185 190
254 Ser Leu Glu Pro Phe Phe Asp Ser Leu Val Lys Gln Thr His Val Pro
255 195 200 205
257 Asn Leu Phe Ser Leu His Leu Cys Gly Ala Gly Phe Pro Leu Asn Gln
258 210 215 220

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